

1/6

AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATGGATTTTGGGCTGATTTTTTTTA 60
1 -----+-----+-----+-----+-----+-----+-----+
TTCGAAATGTCAATGAGTCGTGTGTCCTGGAGTGGTACCTAAAACCCGACTAAAAAAAAT
C A L Q L L S T Q D L T M D F G L I F F I -
TTGTTCTTTTAAAAGGGGTCCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGG 120
61 -----+-----+-----+-----+-----+-----+-----+
AACAAGAAAATTTTCCCCAGGTCTCACTTCACTTCGAACTCCTCAGACCTCCTCCGAACC
C V L L K G V Q S E V K L E E S G G G L V -
TGCAACCTGGAGGATCCATGAAACTCTCCTGTGTAGCCTCTGGATTTACTTTTCACTGGCT 180
121 -----+-----+-----+-----+-----+-----+-----+
ACGTTGGACCTCCTAGGTACTTTGAGAGGACACATCGGAGACCTAAATGAAAGTCACCGA
C Q P G G S M K L S C V A S G F T F S G Y -
ACTGGATGTCTTGGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTA 240
181 -----+-----+-----+-----+-----+-----+-----+
TGACCTACAGAACCCAGGCGGTGAGAGGTCTCTTCCCCGAACTCACCCAACGACTTTAAT
C W M S W V R Q S P E K G L E W V A E I R -
GATTGAAATCTGATAATTATGCAACACATTATGCGGAGTCTGTGAAAGGGAAGTTCACCA 300
241 -----+-----+-----+-----+-----+-----+-----+
CTAACTTTAGACTATTAATACGTTGTGTAATACGCCTCAGACACTTTCCTTCAAGTGGT
C L K S D N Y A T H Y A E S V K G K F T I -
TCTCAAGAGATGATTCCAAAAGTCGTCTCTACCTGCAAATGAACAGCTTAAGAGCTGAAG 360
301 -----+-----+-----+-----+-----+-----+-----+
AGAGTTCTCTACTAAGGTTTTTCAGCAGAGATGGACGTTTACTTGTGAATTCTCGACTTC
C S R D D S K S R L Y L Q M N S L R A E D -
ACAGTGGAGTTTATTACTGTACAGATTTTATAGACTGGGGCCAAGGGACACTAGT 415
361 -----+-----+-----+-----+-----+-----+-----+
TGTCACCTCAAATAATGACATGTCTAAAGTATCTGACCCCGGTTCCCTGTGATCA
C S G V Y Y C T D F I D W G Q G T L -

FIG. 1

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AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATGAGGTTCTCTGTTCAAGTTTCTGG
1 -----+-----+-----+-----+-----+-----+ 60
TTCGAAATGTCAATGAGTCGTGTGTCCTGGAGTGGTACTCCAAGAGACAAGTCAAAGACC
C A L Q L L S T Q D L T M R F S V Q F L G -
GGGTGCTTATGTTCTGGATCTCTGGAGTCAGTGGGGATATTGTGATAACCCAGGATGAAC
61 -----+-----+-----+-----+-----+-----+ 120
CCCACGAATACAAGACCTAGAGACCTCAGTCACCCCTATAACACTATTGGGTCCTACTTG
C V L M F W I S G V S G D I V I T Q D E L -
TCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCCATCTCCTGCAGGTCTAGTAAGAGTC
121 -----+-----+-----+-----+-----+-----+ 180
AGAGGTTAGGACAGTGAAGACCTCTTAGTCAAAGGTAGAGGACGTCCAGATCATTCTCAG
C S N P V T S G E S V S I S C R S S K S L -
TCCTGTATAAGGATGGGAAGACATACTTGAATTGGTTTCTGCAGAGACCAGGACAATCTC
181 -----+-----+-----+-----+-----+-----+ 240
AGGACATATTCTTACCCTTCTGTATGAACTTAACCAAAGACGTCTCTGGTCTCTGTTAGAG
C L Y K D G K T Y L N W F L Q R P G Q S P -
CTCAGCTCCTGATGTATTTGATGTCCACCCGTGCATCAGGAGTCTCAGACCGGTTTAGTG
241 -----+-----+-----+-----+-----+-----+ 300
GAGTCGAGGACTACATAAACTACAGGTGGGCACGTAGTCCTCAGAGTCTGGCCAAATCAC
C Q L L M Y L M S T R A S G V S D R F S G -
GCAGTGGGTCAGGCACAGATTTACCCTGGAAATCAGTAGAGTGAAGGCTGAGGATGTGG
301 -----+-----+-----+-----+-----+-----+ 360
CGTCACCCAGTCCGTGTCTAAAGTGGGACCTTTAGTCATCTCACTTCCGACTCCTACACC
C S G S G T D F T L E I S R V K A E D V G -
GTGTGTATTACTGTCAACAACTTGTAGAGTATCCATTACGTTTCGGGCTCGGGGACAAAGT
361 -----+-----+-----+-----+-----+-----+ 420
CACACATAATGACAGTTGTTGAACATCTCATAGGTAAGTGAAGCCGAGCCCCTGTTTCA
C V Y Y C Q Q L V E Y P F T F G S G T K L -
TGGAATAAAACGTACG
421 ----- 437
ACCTTTATTTTGCATGC
C E I K R T -

FIG. 2

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GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCC
1 -----+-----+-----+-----+-----+ 60
CTATAACACTACTGAGTCAGAGGTGAGAGGGACGGGCAGTGGGGACCTCTCGGCCGGAGG

A [D I V M T Q S P L S L P V T P G E P A S -
69 70 117 118
ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG
61 -----+-----+-----+-----+ 120
TAGAGGACAGCGAGCTCATTCTCAGAGGACATATTCCTACCCTTCTGTATGAACTTAACC

A I S C [R S S K S L L Y K D G K T Y L N] [W -
162 163
TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGATGTCCACCCGGGCA
121 -----+-----+-----+-----+ 180
ATGGACGTCTTCGGTCCCGTCAGAGGTGTCGAGGACTAGATAAAGTACAGGTGGGCCCCGT

A Y L Q K P G Q S P Q L L I Y [L M S T R A -
183 184 CDR2
TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC
181 -----+-----+-----+-----+ 240
AGTCCCCAGGGACTGTCCAAGTCACCGTCACCTAGTCCGTGTCTAAAATGTGACTTTTAG

A S [G V P D R F S G S G T D F T L K I -
279 280 FR3
AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA
241 -----+-----+-----+-----+ 300
TCGTCTCACCTCCGACTCCTACAACCCCAAATAATGACAGTTGTGACCATCTCATAGGT

A S R V E A E D V G V Y Y C [Q Q L V E Y P -
306 307 339 340 CDR3
TTCACGTTTCGGCCAAGGGACCAAGGTGGAGATCAAACGTACGGTGGCT
301 -----+-----+-----+-----+ 348
AAGTGCAAGCCGGTTCCCTGGTTCCACCTCTAGTTTGCATGCCACCGA

A F T [F G Q G T K V E I K R] T V A -
FR4

FIG. 3

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FIG. 4

GAGGTGCACTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCCGGGGTCCCTTAGACT
 1 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
 CTCCACGTCGACCACCTCAGACCCCCTCCGAACCATTTCCGGGCCCCCAGGGAATCTGAG
 FR1
 A [E V Q L V E S G G G L V K P G G S L R L -
 90 91 105 106
 TCCTGTGCAGCTAGCGGATTCACTTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCT
 61 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 120
 AGGACACGTCGATCGCCTAAGTGAAAGTCAACCGATGACCTACAGGACCCAGGCGGTCCGA
 CDR1
 A S C A A S G F T F S [G Y W M S] [W V R Q A -
 147 148
 CCAGGGAAGGGGCTCGAGTGGGTGCTGAAATTAGATTGAAATCTGATAATTATGCAACA
 121 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 180
 GGTCCCTTCCCCGAGCTCACCCAACGACTTTAATCTAACTTTAGACTATTAATACGTTGT
 FR2 CDR2
 A P G K G L E W V A [E I R L K S D N Y A T -
 204 205
 CATTATGCGGAGTCTGTGAAGGGCAAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA
 181 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 240
 GTAATACGCCTCAGACACTTCCCTTTAAGTGGTAGAGTTCTCTACTAAGTTTTAGATCT
 A H Y A E S V K [G] [K F T I S R D D S K S R -
 CTGTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTACAGAT
 241 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 300
 GACATAGACGTTTACTTTGTCGGACTTTTGCTCCTGTGTGGGCACATAATGACATGCTA
 FR3
 A L Y L Q M N S L K T E D T A V Y Y C T D] -
 300 301 309 310 333
 TTCATAGACTGGGGCCAGGGAACACTAGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCA
 301 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 360
 AAGTATCTGACCCCGGTCCCTTGTGATCAGTGGCAGAGGAGTCGGAGGTGGTTCCTGGGT
 CDR3 FR4 CONSTANT REGION
 A [F I D] [W G Q G T L V T] [V S S A S T K G P -
 TCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGC
 361 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 420
 AGCCAGAAGGGGGACCGTGGGAGGAGGTTCTCGTGGAGACCCCGTGTGCGCGGGACCCG
 A S V F P L A P S S K S T S G G T A A L G -
 TGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCTG
 421 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
 ACGGACCAGTTCTGATGAAGGGGCTTGGCCACTGCCACAGCACCTTGAGTCCGCGGGAC
 A C L V K D Y F P E P V T V S W N S G A L -
 ACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGC
 481 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
 TGGTCGCCGCACGTGTGGAAGGGCCGACAGGATGTCAGGAGTCTGAGATGAGGGAGTCG
 A T S G V H T F P A V L Q S S G L Y S L S -
 AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTGAAT
 541 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
 TCGCACCACTGGCACGGGAGGTCGTCGAACCCGTGGGTCTGGATGTAGACGTTGCACTTA
 A S V V T V P S S S L G T Q T Y I C N V N -
 CACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTGGAGCCCAAATCTTGTGACAAAAT
 601 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 660
 GTGTTCTGGGTCGTTGTGGTTCACCTGTTCTTACCTCGGGTTTAGAACACTGTTTTGA
 A H K P S N T K V D K K V E P K S C D K T -
 CACACATGCCACCGTGCCAGCACCTGAACTCGCGGGGGCACCGTCAGTCTTCTCTTC
 661 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 720

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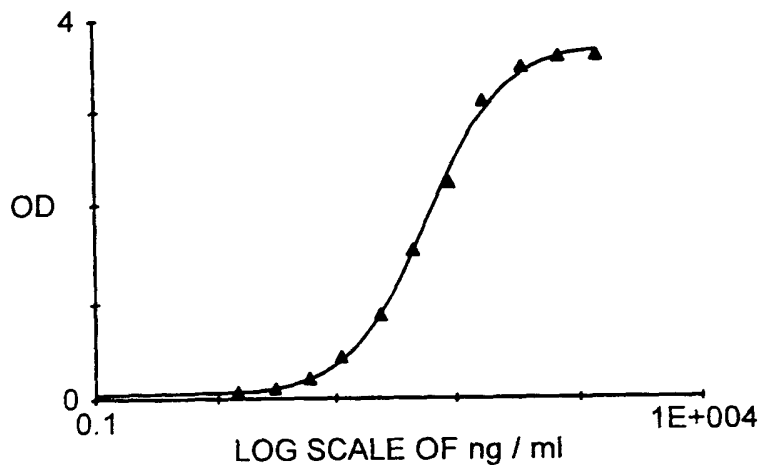
GTGTGTACGGGTGGCACGGGTCGTGGACTTGAGCGCCCCCGTGGCAGTCAGAAGGAGAAG
A H T C P P C P A P E L A G A P S V F L F -
721 CCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTG
-----+-----+-----+-----+-----+ 780
GGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGACGCACCAC
A P P K P K D T L M I S R T P E V T C V V -
781 GTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG
-----+-----+-----+-----+-----+ 840
CACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTC
A V D V S H E D P E V K F N W Y V D G V E -
841 GTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTG
-----+-----+-----+-----+-----+ 900
CACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAG
A V H N A K T K P R E E Q Y N S T Y R V V -
901 AGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTC
-----+-----+-----+-----+-----+ 960
TCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTCCTCATGTTACGTTCCAG
A S V L T V L H Q D W L N G K E Y K C K V -
961 TCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCC
-----+-----+-----+-----+-----+ 1020
AGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGG
A S N K A L P A P I E K T I S K A K G Q P -
1021 CGAGAACCACAGGTGTACACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTC
-----+-----+-----+-----+-----+ 1080
GCTCTTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAG
A R E P Q V Y T L P P S R D E L T K N Q V -
1081 AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGC
-----+-----+-----+-----+-----+ 1140
TCGGACTGGACGGACCAAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCG
A S L T C L V K G F Y P S D I A V E W E S -
1141 AATGGGCAGCCGGAGAACAACACTACAAGACCACGCTCCCGTGCTGGACTCCGACGGCTCC
-----+-----+-----+-----+-----+ 1200
TTACCCGTCGGCCTCTTGTTGATGTTCTGGTGGGAGGGCACGACCTGAGGCTGCCGAGG
A N G Q P E N N Y K T T P P V L D S D G S -
1201 TTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC
-----+-----+-----+-----+-----+ 1260
AAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAG
A F F L Y S K L T V D K S R W Q Q G N V F -
1261 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG
-----+-----+-----+-----+-----+ 1320
AGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGAC
A S C S V M H E A L H N H Y T Q K S L S L -
1321 TCTCCGGGTAAATGA
-----+-----+-----+ 1335
AGAGGCCCATTTACT
A S P G K * -

FIG. 4 CONT'D

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$$y = (A - D) / (1 + (x/C)^B) + D$$

A=0.0501 B=1.31 C=60.3 D=3.74

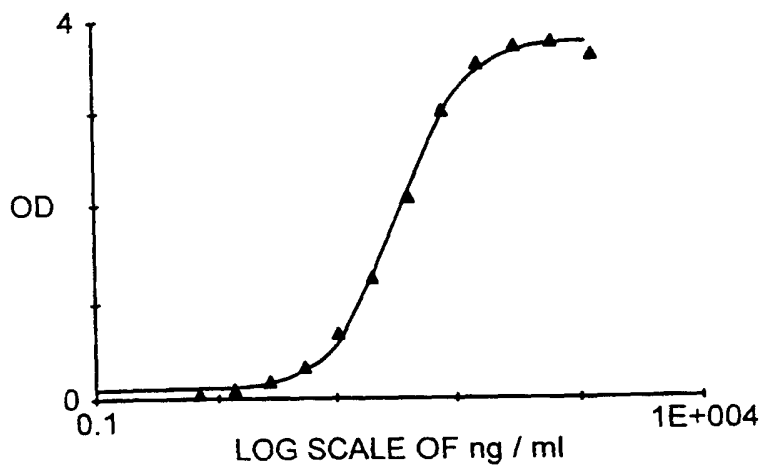


CHIMERIC CD23 IgG1m
HALF MAXIMUM BINDING=16.28ng/ml

FIG. 5

$$y = (A - D) / (1 + (x/C)^B) + D$$

A=0.104 B=1.49 C=37.7 D=3.78



HUMANIZED CD23 IgG1m
HALF MAXIMUM BINDING=15.03ng/ml

FIG. 6